IN THE CLAIMS

Please amend claims 1, 6, 29 and 30 and add claim 39 as indicated in the complete listing of all claims in the application set forth below.

Claim 1. (Currently Amended) An isolated DNA sequence comprising a nucleic acid sequence that is SEQ ID NO: 1 and a complementary sequence thereof.

Claim 2. (Original) The isolated nucleic acid of claim 1, wherein said nucleic acid is cDNA.

Claims 3-5. (Canceled)

Claim 6. (Currently Amended) An isolated oligonucleotide ~~of at least 8 consecutive nucleotides~~ selected from a sequence unique to ~~SEQ ID NO: 1 or~~ the complement of SEQ ID NO: 1~~, namely an oligonucleotide of SEQ ID NO: 3 or SEQ ID NO: 4~~.

Claim 7. (Original) The oligonucleotide of claim 6, wherein the oligonucleotide is a member of an oligonucleotide pair for amplification of an HH nucleic acid sequence.

Claims 8-28. (Canceled)

Claim 29. (Currently Amended) A genetic marker predictive of a hereditary hemochromatosis (HH) gene mutation comprising a partial sequence of SEQ ID NO: 1 having a single nucleotide substitution of A-to-C at position 734 (A734C) in exon 5 in comparison with non-mutated SLC11A3 and sequences complementary therewith~~, namely an oligonucleotide of SEQ ID NO: 3 or SEQ ID NO: 4~~.

Claim 30. (Currently Amended) A method for diagnosing an individual ~~patient~~ as having an increased risk of developing HH disease, comprising:

providing the isolated DNA sequence of claim 1 from the individual; and

assessing the isolated DNA sequence for the presence or absence of a base mutation at position 734 (A734C) of the SLC11A3 gene, wherein the presence ~~absence~~ of the A base ~~mutation~~ indicates the absence of a HH gene mutation in the genome of the individual and the presence of the C base mutation indicates the presence of the HH gene mutation and an increased risk of developing HH disease in the genome of the individual being diagnosed.

Claim 31. (Previously Presented) The method of claim 30, wherein the assessing step is performed by a process which

comprises subjecting the isolated DNA sequence to amplification using oligonucleotide primers flanking the base-pair mutation.

Claim 32. (Previously Presented) The method of claim 31, wherein the assessing step further comprises an oligonucleotide ligation assay.

Claims 33-38. (Canceled)

Claim 39. (New) A kit for diagnosing an individual as having an increased risk of developing HH disease, comprising:

a means for providing the isolated DNA sequence of claim 1 from the individual;

a means for assessing the isolated DNA sequence for the presence or absence of a base mutation at position 734 (A734C) of the SLC11A3 gene, wherein the presence of the A base indicates the absence of a HH gene mutation in the genome of the individual and the presence of the C base mutation indicates the presence of the HH gene mutation and an increased risk of developing HH disease in the genome of the individual being diagnosed; and